

SEQUENCE LISTING

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 AURORA BIOSCIENCES CORPORATION
 TSIEN, Roger
 HEIM, Roger
 CUBITT, Andrew

<120> TANDEM FLUORESCENT PROTEIN CONSTRUCTS

<130> REGEN1260-3

<150> US 08/792,553

<151> 1997-01-31

<150> US 09/396,003

<151> 1999-09-13

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 716

<212> DNA

<213> *Aequorea victoria*

<220>

<221> CDS

<222> (1)..(714)

<223>

<400> 1

atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt 48
 Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cgg 240
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att 384

1057505.012502

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct 576
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tgg 624
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta 672
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa ta 716
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235
 <210> 2
 <211> 238
 <212> PRT
 <213> Aequorea victoria
 <400> 2
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

10057505.012502

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 3
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 3

Ser Gln Asn Tyr Pro Ile Val Gly
 1 5

<210> 4
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 4

10057505.012502

Lys Ala Arg Val Leu Ala Glu Ala Met Ser
1 5 10

<210> 5
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Linker moiety

<400> 5

Pro Ser Pro Arg Glu Gly Lys Arg Ser Tyr
1 5 10

<210> 6
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Linker moiety

<400> 6

Tyr Val Ala Asp Gly
1 5

<210> 7
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Linker moiety

<400> 7

Met Phe Gly Gly Ala Lys Lys Arg
1 5

<210> 8
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Linker moiety

<400> 8

Gly Val Val Asn Ala Ser Ser Arg Leu Ala
1 5 10

10057505.012502

<210> 9
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 9

Leu Ile Ala Tyr Leu Lys Lys Ala Thr
 1 5

<210> 10
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 10

Val Lys Met Asp Ala Glu Phe
 1 5

<210> 11
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 11

Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg
 1 5 10 15

His

<210> 12
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 12

Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His
 1 5 10

<210> 13

205210"50525001

<211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 13

Lys Pro Ala Leu Phe Phe Arg Leu
 1 5

<210> 14
 <211> 30
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 14

Gln Pro Leu Gly Gln Thr Ser Leu Met Lys Arg Pro Pro Gly Phe Ser
 1 5 10 15

Pro Phe Arg Ser Val Gln Val Met Lys Thr Gln Glu Gly Ser
 20 25 30

<210> 15
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Cleavage recognition sequence

<400> 15

Gly Gly Gly Gly Ser
 1 5

<210> 16
 <211> 22
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 16

Gly Gly Gly Gly Gly Ser Met Phe Gly Gly Ala Lys Lys Arg Ser
 1 5 10 15

Gly Gly Gly Gly Gly
 20

10057505.012503

<210> 17
 <211> 35
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 17

Ile Gln Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser
 1 5 10 15

Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val
 20 25 30

Gly Glu Arg
 35

<210> 18
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 18

Ser Lys Val Ile Leu Phe
 1 5

<210> 19
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer sequence

<400> 19
 ggatccccc gctgaattca tg

22

<210> 20
 <211> 15
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer sequence

<400> 20
 aaataataag gatcc

15

10057505.012502

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer

 <400> 21
 ggtaagcttt tatttgtata gttcatccat gcc 33

<210> 22
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer sequence

 <400> 22
 agaaaggcta gcaaaggaga agaa 24

<210> 23
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer sequence

 <400> 23
 tcagtctaga ttgtatagt tcatc 25

<210> 24
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fusion sequence

<400> 24
 Met Arg Gly Ser His His His His His His
 1 5 10

<210> 25
 <211> 25
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker moiety

<400> 25

205210-50525001

Ser Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp
 1 5 10 15

Asp Asp Lys Asp Pro Pro Ala Glu Phe
 20 25

<210> 26
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker sequence

<400> 26

Ala Asn Pro Leu Tyr Lys Asp Ala Thr Asp Phe Thr
 1 5 10

<210> 27
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker sequence

<400> 27

Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Asp Phe Thr
 1 5 10

<210> 28
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker sequence

<400> 28

Gly Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Gly Asp Phe Thr
 1 5 10 15

<210> 29
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker sequence

<400> 29

Gly Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Gly Ser Thr Asp

10057505.012502

1

5

10

15

Phe Thr

<210> 30

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> Linker sequence

<400> 30

Gly Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Gly Ser Thr Gly

1

5

10

15

Ser Asp Phe Thr

20

<210> 31

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> Linker sequence

<400> 31

Gly Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Gly Ser Thr Gly

1

5

10

15

Ser Gly Ser Asp Phe Thr

20

10057505-012507